REMARKS

The substitute Sequence Listing includes sequences recited in claims 9, 31, 41, and 54, mentioned by the Examiner in the Office communication, dated July 30, 2001, and Notice of Abandonment, mailed January 16, 2002. The Specification has been amended to include sequence identification numbers for sequences presented in Table 5 and in the forementioned claims.

Attached hereto is a marked-up version of the changes made to the Specification and Claims by the current amendment. The attached page is captioned **"Version with markings to show changes made."**

The undersigned hereby states that the computer-readable form copy (CRF copy) of the substitute Sequence Listing and the paper copy of the substitute Sequence Listing, submitted in accordance with 37 C.F.R. § 1.825(a) and (b), respectively, are the same and contain no new matter. Accordingly, entry of the substitute Sequence Listing into the above-captioned case is respectfully requested.

In the unlikely event that the transmittal letter is separated from this document and the Patent Office determines that an extension and/or other relief is required, applicants petition for any required relief including extensions of time and authorize the Assistant Commissioner to charge the cost of such petitions and/or other fees due in connection with the filing of this document to **Deposit Account No. 03-1952** referencing Docket No. 399632000820. However, the Assistant Commissioner is not authorized to charge the cost of the issue fee to the Deposit Account.

Respectfully submitted,

Dated: February 19, 2002 By: _____

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Table 5 has been amended as follows:

Peptide	AA	Sequence	SEQ ID NO	Antigen	Protein or Molecule	1st Position	A*0201
1317.02	8	ALPPVAPV	107	P53		69	0.0230
1317.11	11	LLPENNVLSPV	108	P53		25	0.1300
F136.02	9	SLYNTITVL	109	HIV	gag	77	0.0330
F136.03	9	SLYNTISVL	110	HIV	gag	77	0.0190
F136.04	9	SLYNTVSTL	111	HIV	gag	77	0.0320
32.0005	9	AIYGRPVSA	112	KSHV		508	0.0560
32.0006	9	ALIGTMCGI	113			237	0.1500
32.0008	9	ATLGTVILL	114	KSHV		8	0.0280
32.0016	9	FIALNLSFI	115	KSHV		624	0.0640
32.0017	9	FIQNIDFKA	116	KSHV		631	0.1400
32.0019	9	FLNSSNLFT	117	KSHV		560	0.0780
32.0021	9	FLYVVCSLA	118	KSHV		2	1.1000
32.0022	9	FVAVHVPDV	119	KSHV		8	0.2600
32.0027	9	GILGTIIFA	120	KSHV		244	0.0270
32.0033	9	HLDFWHHEV	121	KSHV		168	0.2400
32.0042	9	ITATFTAPL	122	KSHV		342	0.1300
32.0050	9	LLGTWMFSV	123	KSHV		53	1.5000
32.0053	9	LMWYELSKI	124	KSHV		492	0.0670
32.0060	9	MIIIVIAII	125	KSHV		738	0.0150
32.0066	9	NLLDRLLLI	126	KSHV		77	0.0290
32.0073	9	RIFYNILEI	127	KSHV		20	0.0800
32.0074	9	RLASSVFDL	128	KSHV		649	0.0670
32.0076	9	RLGAIPPLV	129	KSHV		24	0.0150
32.0078	9	RLYQASAVM	130	KSHV		4	0.0180

Peptide	AA	Sequence	SEQ ID NO	Antigen	Protein or Molecule	1st Position	A*0201
32.0081	9	SILGCDVSV	131	KSHV		226	0.0430
32.0087	9	SVDFYQFRV	132	KSHV		59	0.0160
32.0088	9	SVSDFDLRI	133	KSHV		245	0.0120
32.0090	9	TLGTVILLV	134	KSHV		9	0.0830
32.0099	9	YLVWQPMSA	135	KSHV		398	0.0130
32.0114	10	AAVEQILTSV	136	KSHV		237	0.0210
32.0118	10	ALIGTMCGIL	137	KSHV		237	0.0120
32.0120	10	ATLGTVILLV	138	KSHV		8	0.0690
32.0124	10	FLYVVCSLAV	139	KSHV		2	0.2400
32.0127	10	GALPICSFVV	140	KSHV		27	0.0160
32.0137	10	KLLGTWMFSV	141	KSHV		52	1.6000
32.0148	10	OLASILGCDV	142	KSHV		223	0.0160
32.0150	10	RLSNRICFWA	143	KSHV		164	0.0130
32.0154	10	SLVTGFINFI	144	KSHV		720	0.0210
32.0159	10	VLATDVTSFL	145	KSHV		149	0.0190
32.0160	10	VLLNGWRWRL	146	KSHV		16	0.2800
32.0164	10	YLVWQPMSAI	147	KSHV		398	0.0230
34.0006	8	QLAKTCPV	148	P53		136	0.0110
34.0132	9	ALBRWGLLV	149	HER2/ neu		5	0.0960
34.0133	9	ALCRWGLLV	150	HER2/ neu		5	0.0360
34.0134	9	AMCRWGLLV	151	HER2/ neu		5	0.0280
34.0135	9	KLFGSLAFL	152	HER2/ neu		369	0.1200
34.0136	9	KLFGSLAFV	153	HER2/ neu		369	0.0900
34.0137	9	KMFGSLAFL	154	HER2/ neu		369	0.2000
34.0138	9	KMFGSLAFV	155	HER2/ neu		369	0.1200
34.0140	9	KMFBQLAKV	156	P53		132	0.0980

Peptide	AA	Sequence	SEQ ID NO	Antigen	Protein or Molecule	1st Position	A*0201
34.0141	9	KMFCQLAKV	157	p53		132	0.0400
34.0199	10	RMPEAAPPVV	158	p53		65	0.0340
34.0201	10	ALNKMFCQLV	159	p53		129	0.0240
35.0031	9	VLLVSLGAI	160	Flu	HEMA	542	0.0170
35.0034	9	LLTEVETPI	161	Flu	VMT2	3	0.2100
35.0036	9	RLIQNSLTI	162	Flu	VNUC	55	0.0300
35.0040	9	KMNIQFTAV	163	Flu	HEMA	402	0.0330
35.0046	10	GLFGAIAGFI	164	Flu	HEMA	345	0.0451
35.0047	10	KLESMGIYQI	165	Flu	HEMA	521	0.0120
35.0048	10	SLPFQNIHPV	166	Flu	HEMA	306	0.0520
37.0013	8	ALPPVAPV	167	p53		69	0.0500
37.0015	9	ALNKMFCQV	168	p53		129	0.0770
37.0017	9	KLFCQLAKV	169	p53		132	0.0640
37.0018	9	KLCPVQLWV	170	p53		139	0.0440
37.0019	9	CLTIHYNYV	171	p53		229	0.0110
37.0032	10	ALNKMFCQLV	172	p53		129	0.0150
37.0033	10	VLVPYEPPEV	173	p53		216	0.1100
37.0034	10	RLPEAAPPVV	174	p53		65	0.0350
37.0035	10	LLPPQHLIRV	175	p53		188	0.0120
37.0069	11	ILLEDSSGNLV	176	p53		255	0.0590
F124.03	10	KLVALGINAV	177	HCV	NS3	1406	0.0110
F124.04	9	SLMAFTAAV	178	HCV	NS4	1789	0.1900
F124.06	9	CINGVCWTV	179	HCV	NS3	1073	0.0910
F124.08	9	TISGVLWQV	180	HCV	NS3	1073	0.1400
F124.09	9	SISGVLWQV	181	HCV	NS3	1073	0.1400
F124.10	9	SLMAFTASV	182	HCV	NS4	1789	0.1200
F124.11	9	GLRDCTMLV	183	HCV	NS5	2727	0.0120
F124.12	10	KLVALGVNAV	184	HCV	NS3	1406	0.0200
F124.14	10	KLSGLGLNAV	185	HCV	NS3	1406	0.0170
F124.23	10	KLVSLGVNAV	186	HCV	NS3	1406	0.0150
F127.03	10	LLALLSCLTV	187	HCV	Core	178	0.0240

Peptide	AA	Sequence	SEQ ID NO	Antigen	Protein or Molecule	1st Position	A*0201
F127.06	9	LLCPAGHAV	188	HCV	NS3	1169	0.0140
F127.07	10	KLVALGINAV	189	HCV	NS3	1406	0.0700
F127.08	9	SLMAFTAAV	190	HCV	NS4	1789	6.5000
F127.09	9	LLFNILGWV	191	HCV	NS4	1807	1.7000

In the Claims:

Claims 9, 31, 41, and 54 have been amended as follows:

9. (Amended) A method of inducing an immune response with a peptide comprising an epitope consisting of about 8-11 residues (SEQ ID NOS: 192, 193, 194, 195) that will bind to an HLA-A2.1 molecule and induce an HLA-A2.1-restricted cytotoxic T cell response, said method comprising steps of:

providing a peptide comprising a putative T cell epitope, said putative epitope comprising a structural motif associated with peptide binding to HLA-A2.1, said structural motif comprising a first anchor amin acid at position two from an N-terminus of the epitope, said first anchor selected from the group consisting of V, A, and T, and a second anchor amino acid selected from the group consisting of L, I, V, M and A at a carboxyl-terminus of the epitope, said peptide connected to another molecule to create a compound with a *proviso* that neither said peptide, said another molecule nor said compound comprise an entire native antigen;

complexing the provided peptide, or a fragment thereof which comprises the epitope, with and HLA molecule; and,

contacting a cytotoxic T lymphocyte (CTL) with the complex, whereby a CTL response is induced.

31. (Amended) A method of inducing an immune response, said method comprising steps of:

obtaining a peptide comprising an epitope (SEQ ID NOS: 192, 193, 194, 195) that comprises an amino acid V, A, or T at a position two relative to an amino terminus of the epitope,

and L, I, V, M, or A at a carboxyl terminus of the epitope, wherein said peptide comprises a binding affinity for an HLA-A2.1 molecule such that a ratio of an IC_{50} of a standard peptide to an IC_{50} of the peptide is at least 0.01, said peptide connected to another molecule to create a compound, with a *proviso* that neither the obtained peptide, the another molecule nor the compound comprise an entire native antigen;

complexing the peptide with an HLA molecule; and,

contacting a cytotoxic T lymphocyte (CTL) with the peptide-HLA complex, whereby a CTL response is induced.

41. (Amended) A method of inducing a human immune response *in vivo* with a peptide comprising an epitope (SEQ ID NOS: 192, 193, 194, 195) consisting of about 8-1 residues that will bind to an HLA-A2.1 molecule and induce an HLA-A2.1-restricted cytotoxic T cell response, said method comprising steps of:

providing a therapeutically effective human dose of a peptide comprising a putative T cell epitope and a pharmaceutical carrier, said putative epitope comprising a structural motif associated with peptide binding to HLA-A2.1, said structural motif comprising a first anchor amino acid at position two from an N-terminus of the epitope, said first anchor selected from the group consisting of V, A, and T, and a second anchor amino acid selected from the group consisting of L, I, V, M, and A at a carboxyl-terminus of the epitope, with a *proviso* that said peptide does not comprise an entire native antigen;

complexing the provided peptide, or a fragment thereof which comprises the epitope, with an HLA molecule *in vivo* in a human; and,

contacting a cytotoxic T lymphocyte (CTL) with the complex *in vivo* in a human, whereby a CTL response is induced.

54. (Amended) A method of inducing a human immune response *in vivo*, said method comprising steps of:

providing a therapeutically effective human dose of a peptide in a pharmaceutical carrier, said peptide comprising an epitope (SEQ ID NOS: 192, 193, 194, 195) that comprises an amino acid V, A, or T at a position two relative to an amino terminus of the peptide comprises a binding affinity such that the ratio of an IC_{50} of the peptide is at least 0.01, with a *proviso* that an obtained peptide is not an entire native antigen;

complexing the peptide with an HLA molecule *in vivo* in a human; and,

contacting a cytotoxic T lymphocyte (CTL) with the peptide-HLA complex *in vivo* in a human, whereby a CTL response is induced.